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version 5.1.6
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  GenCore
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- nucleic search, using sw model OM nucleic

Run on:

April 14, 2005, 14:06:59 ; Search time 562 Seconds (without alignments) 10263.124 Million cell updates/sec

US-10-018-105-3 3525

score:

Scoring table: Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC

1202784 seqs, 818138359 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:/cgn2\_6/ptodata/1/ina/backfiles1.seq: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: Issued Patents NA:

Pred. No. is the number of results predicted by chance to becore greater than or equal to the score of the result beir and is derived by analysis of the total score distribution.

						SUMMARIES		
Res	Result No.	Score	Query Match	Query Match Length	DB.	ΩI	Description	uc
!	-	2155.2	61.1	2358	4	US-09-248-796A-6328	Sequence	6328, Ar
	N	423.8	12.0	507	4	US-09-248-796A-6327	Seguence	6327, Ar
υ	m	168.2	4.8	537	ო	US-08-998-416-66	Sequence	66, At
	4	118.2	3.4	2445	4	US-09-248-796A-6302	Sequence	6302, Ar
	Ŋ	73.4	2.1	. 708	4	US-09-248-796A-10622	Sequence	10622, 7
	9	71.8	5.0	19124	~	US-08-487-826B-13	Sequence	13, Appl
	7	68.8	2.0	1141	4	US-09-806-708B-22	Sequence	22, Appl
	80		1.9	767677	4	US-09-949-016-12147	Sequence	12147, 7
	σ	68	1.9	767677	4	US-09-949-016-17361	Sequence	17361, 7
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O	12	8.99	1.9	14066	4	US-09-601-198-56	Sequence	56, Appl
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U	14	99	1.9	26000	4	US-09-843-376-10	Sequence	
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υ	16	65.8	1.9	205044	4	US-09-949-016-15852	Sequence	15852, 7
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U	20	65.8	1.9	223471	4	US-09-949-016-12725	Sequence	
	21	65.2	1.8	1037	4	US-09-181-585-3	Sequence	
	22	65.2	1.8	1159	4	US-09-181-585-1	Sequence	1, Appli
	23	65.2	1.8	1471	4	US-09-181-585-2	Sequence	
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U	<b>5</b> 6	63.6	H.	119153	4	US-09-949-016-12378	Sequence	123
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28 63.4 1.8 187169 4 US-09-949-016-12776 Sequence 12776, A 18 1811819 4 US-09-949-016-15940 Sequence 15940, A 2 0 62.4 1.8 114194 4 US-09-949-016-15940 Sequence 15940, A 2 0 62.4 1.8 114194 4 US-09-949-016-16997 Sequence 16997, A C 32 61.8 1.8 129415 4 US-09-949-016-16997 Sequence 16997, A C 33 61.4 1.7 187169 4 US-09-949-016-12740 Sequence 15940, A C 34 61.4 1.7 191569 4 US-09-949-016-12940 Sequence 12776, A C 35 61.2 1.7 3095 6 5231168-1 Parent No. 5231168-1 Parent														,			
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28 63.4 1.8 18 30 62.4 1.8 19 31 61.8 1 18 12 32 61.8 1 18 12 33 61.8 1 18 12 34 61.4 1.7 18 35 61.2 1.7 18 36 61.2 1.7 18 39 61 1.7 19 41 60.8 1.7 45 45 60.6 1.7 45	US-09-949-016-12776 US-09-949-016-15940	US-09-949-016-16536	US-09-949-016-16997	US-09-949-016-14624	US-09-949-016-12776	US-09-949-016-15940 4	. US-08-451-405A-2	5231168-1	5231168-1	US-09-949-016-379	US-09-949-016-4309	US-09-949-016-12928	US-09-949-016-12740	US-09-949-016-12896	US-09-949-016-17305	US-08-998-416-186	US-09-902-540-1280
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### ALIGNMENTS

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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBACE: 107196,132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR PAPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6228
LENGTH: 2358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAGTGAAAGTTATTATCAAAATTCAACTACTAATCAACCTATTCTTAGATCTGATGAAG 118
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Pred. No. 0;
0; Mismatches
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            Sequence 6328, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
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Best Local Similarity 97.2%;
Matches 2293; Conservative
                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; Candida albicans
US-09-248-796A-6328
-09-248-796A-6328
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CTGGTTCTTCAATTAAGAAAAATCTAATCTTACCGATAAAGATAGAATTACCAACCCTA 358

; FILE REFEREN	_	1892 CCCCCGATATTCCATCATTAGTATCACCAGGTCAATCTGTTCGAGATTTATTT	
		GAGGITCATTACCTGATAGATTTTCACTTTTCCATTCTGAATCAGAAGAAACTATTCATG	13
<pre>// Patent No. 674 // GENERAL INFORM // APPLICANT: KA</pre>	•	)2 GAGGITCAITACCIGAIAGAITITICACITITICCAITCIGAATCAGAAACIAITICAIG 1691	W. 1632
RESULT 2 US-09-248-796A-1 ; Sequence 6327		2 CTGGATCTGGATCTGGGCAGGTGAAATTTGGTGGAGCAAGAATTTCTGATGGGATTAATG 1631 	Qy 1572 Ub 1319
Db 2336 .A		CACCITACAATATGATGATCAATTATCATTAACTTCATCTACATCTTCTACGAT	
Oy 2586 A			_
		TTACTCATGAAAATTCTTCATCTTCAGAAGAAATTTATGAATTGAAGACTAAACAACAAC TTACTCATGAAAATTCTTTCATCTTCAGAAAATTTATGAATTGAAGACTAAACAACAACAACAACAAACA	Oy 1458
2526		TGGCAGCATTAAAATATACTCCAAAAAATATTTTAAAGAAAACATTATCAAGATTTGAAT	
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Oy 2172 A		01 CTGATTCTCATGCATCAAGATCATCTCAAGAAACTGAAGAAGATGTTTGTT	Qy 1101
Db 1859 T			UD 179
Qy 2112 T		AACTIGGIACIACAACCCTIGGIGTIGGAACTIGGIACTACCGCCACTG	•
UY 2052 A     Db 1799 A		AACTIGGTATTGGTGCTACAACCCTTGGTGTTGGAACTGGTACTACCGCCACTGCCACTG	
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 Db 1679 A		873 CAATTGGTCGTAATAATTCTAATAATTTGAAATGATTTAGTTAG	.s .s.
UD 1619 A		539 CTANTAAATCAAGAAAATCTCAATTGGAAAATTTACCTCCATTAATTA	Db 40
Oy 1872 A		87	.8 8
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Ov 1812 C		419 TGAGTICATTACGTAAAGATTTTTATTTAAAAGATAATACTGACGACAATTCTACTAATA 478	Db 4.
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                                               CCAAAGCATTIGGTATICATCCTTTAACTGCTGAAGATATTCGAATGCAAGAAACTCGTG
                                                                                                                            CAAGAAGAAAAGTCATGACTTTAATGAGATTATTATCAGGTAAAGCTGATGTCATTAAAA
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7, Application US/09248796A 747137

NEWATION: Keith Weinstock et al VERTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE VERTION: FOR DIAGNOSTICS AND THERAPEUTICS NUCE: 107196.132

OM nucleic - nu	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model
Run on:	April 14, 2005, 13:36:05 ; Search time 1739 Seconds (without alignments) 11999.476 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-018-105-3 3525 1 tatataatatatatatatatatcaattattatcaatattgc 3525
Scoring table:	IDENTITY NUC Gapox 1.0
Searched:	4390206 segs, 2959870667 residues
Total number of	Total number of hits satisfying chosen parameters: 8780412
Minimum DB seg ] Maximum DB seg ]	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

geneseqn2000s:\* geneseqn2001as:\* geneseqn2003as: Geneseq\_16Dec04: geneseqn1990s:\* geneseqn2003cs geneseqn2004bs genesegn2002as geneseqn2001bs geneseqn2002bs geneseqn2003bs Database

Post-processing: Minimum Match 0\*
Maximum Match 100\*
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description				Abtional Action	•	<b>,</b> (	٠.			Abz10246 Haematopo	_	Abt20615 Aspergill	Abt18799 Aspergill			٠,	TITETHER SYSTEM	Aberran OKF	ADG/210/ Anopheles	Act79720 Mosquito	Aaf07924 Fusarium	
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# ALIGNMENTS

Candida albicans; yeast pathogen; identification; fungal; antifungal; CaKRBS; CaALR1; CaCDC24; diagnosis; fungicide; fungal infection; ds. Candida albicans CaALR1 nucleotide sequence. RESULT 1 AAC87954 ID AAC87954 standard; DNA; 3525 BP. Davison J; (MYCO-) MYCOTA BIOSCIENCES INC. 05-MAY-2000; 2000WO-CA000533. 99US-0132878P. (first entry) Roemer T, Bussey H, Candida albicans. WO200068420-A2. 06-MAR-2001 05-MAY-1999; 16-NOV-2000. AAC87954;

WPI; 2000-687652/67. P-PSDB; AAB36515.

New DNA encoding essential proteins of Candida albicans, useful for diagnosing fungal infections and to screen for clinical or agricultural antifungal agents.

Claim 3; Fig 2A; 76pp; English.

The present sequence represents the fungus-specific Candida albicans gene-CaALR1. The present invention describes the fungus-specific genes CaKRES, CaALR1 and CaCDCC4 isolated in the yeast pathogen C. albicans. The genes have antifungal and fungicide activity. The genes in C. albicans and are useful as drug targets. Fragments of them are useful as probes and primers for diagnosis of fungal infections, also as antisense and ribozyme agents. Proteins encoded by the genes are used to screen for

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their specific inhibitors which are potential antifungal agents for controlling a wide range of fungi pathogenic on animals or plants. Fragments of the proteins are also used to raise specific antibodies. Higher animals do not contain genes closely similar to the C. albicans genes, so antifungal agents that target them are less likely to be toxic to humans
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JP 2002543799-A/2
24-DEC-2002
05-MAY-1999 US 60/132878
TERRY ROEMER, HOWARD BUSSEY, JOHN DAVISON
C12N15/09, C07K14/40, C07K16/14, C12Q1/68, G01N33/15, G01N33/50, PC
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I (bases 1 to 325)
Roemer T., Bussey, H. and Davison, J.
Identification of candida albicans essential fungal specific genes and use thereof in antifungal drug discovery
Patent: JP 2002543799-A 2 24-DEC-2002;
MCGILL UNIVERSITY
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Saccharomycetales, mitosporic Saccharomycetales, Candida.
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Query Match

99.9%; Score 3523; DB 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3525; Conservative 0; Mismatches 0;

AB004538 Schizosac CR382130 Yarrowia Z99162 S.pombe chr

AB004538 CR382130\_00 SPAC17G6

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**AB004539** 

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CQ446161 Sequence AL021766 S.pombe c AB004539 Schizosac

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 /organism="Candida albicans" /mol\_type="genomic DNA"
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TGAAAATGATTTAGTTAGTCCCATGACAAAATGAAAACTAATGATAGTGAAGATATTAC 960 	<b>상</b> 옵	1981 CCATGATGGTATTAACGTTCCATTTTTCACCAATTTCTCATCCAGCAAATGTTAGAAG 2040 
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161	TGGAGAGTAGGAGTAGGAATTAATTTTGGTCCCAATCCAACTGGAAATAATACTAA TGGAGAGTAGGAGTAGGAATTAATTTTGGTCCCAATCCAACTGGAAATAATACTAA TGGAGAGTAGGAGGAATTAATTTTTGGTCCCAATCCAACTGGAAATAATACTAA TACTAATACTAATACTACTGGTTCACCTTCACCCCCAACCAA	TTTCAGTCGTTCACATTCTAAAATTTACTCAATTACAAGTCGAACTTCAATTCCAA TAATAAAATCACCGAAATGTTTTCTAAAATTACTTCATTGATTG	2941 AITTCCTCANTGGTGGTTGAAAAATTGAATTGAATTGAAGGCACAAATAATGGTAA 3000 3001 TCGACCAATTTTTAATCATTCATCAAGAAGATCAATTAGAAGTTTAAGGTTTAAAAAAACA 3060 3001 TCGACCAATTTTTAATCATTCATCAAGAAGATCAATTAGAAGTTTAAGGTTTAAAAAAACA 3060 3061 TGGTGGTAATTAATCATTCATCAAGAAGATCAATTAGAATTAAGAATAATCAAAAAAAA

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0; Mismatches 23; Indels
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                                                                                                                                                                  Sequence 6328 from patent US 6747137.
AR551197.1 GI:53944372
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Weinstock, K.G. and Bush, D.
Nucleic acid sequences relating to Cam
and therapeutics
Patent: US 6747137-A 6328 08-JUN-2004;
Location/Qualifiers
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Total number of hits satisfying chosen parameters:

68479088

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\*
Maximum Match 100\*
Listing first 45 summaries

EST:\* Database :

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SUMMARIES		ei ei	CNS06173	CNS0736W	CNS06QJK	CNS072G5	BZ295013	CNS06HIN	CNS06GW9	CNS06GN7	C0028936	C0142543	CF709049	CNS06GSK	BZ297820	AJ637812	BM266292	BQ743184	C0034119	CD488599 .	CNS06X53	CNS075PZ	C0027928	CNS06H1J	CF823927	AJ637804
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		Length DB	912	1032	1089	798	579	911	874	911	955	387	771	973	524	763	614	712	964	715	. 850	921	907	895	934	551
*		Match	10.2	8.6	6.0	6.0	5.7	5.3	5.0	5.0	4.9	4.6	4.4	4.1	4.1	4.1	4.0	4.0	3.8	3.6	ы 5	3.5	3.4	H	3.3	3.1
		Score	359.8	301.6	211.2	210.8	202	187.2	176	176	172.4	163	156.2	146	145.4	143	141.2	141	133.2	128.4	122.6	121.8	119.2	117	114.8	110.2
٠	Result	No.	0	0	m	Ω	n 5	9	7	60	6	10	11	12	13	14	15	16	c 17	18	19	50	c 21.	22	c 53	24

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	CF709038	AL440364	C0011480	CF820256	AQ946120	BZ780846	CF715298	CG403581	C0025755	C0025396	C0028288	C0025732	C0031086	C0028935	BQ491813	BH873429	BX145762	BH391984	CF816703	A0940248	BZ388480
							3														
	CF/09038	CNS07DEE	CO011480	CF820256	AQ946120	B2780846	CF715298	CG403581	C0025755	C0025396	C0028288	C0025732	C0031086	C0028935	BQ491813	BH873429	BX145762	BH391984	CF816703	AQ940248	BZ388480
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Č	98/	1001	901	965	641	575	819	. 707	815	823	907	932	. 936	686	413	587	781	. 832	772	700	670
	1.0	3.1	3.1	3.1	0°E	3.0	5.9	2.9	2.9	2.9	2.9	5.9	2.9	2.9	2.8	2.8	2.8	2.8	2.7	2.7	2.7
,	# · · · ·	108.6	108.2	108	106.6	106	102.4	102.2	100.6	100.6	100.6	100.6	100.6	100.6	100.4	8.66	8.66	97.4	96.2	96	95.4
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## ALIGNMENTS

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 18:55:46; Search time 1925 Seconds ("without alignments)

Title: US-10-018-105-3

Perfect score: 35.5

Sequence: 1 tatatatatatatatatata......tcaattattatcaatattgc 35.5

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum Match 100*

Maximum Match 100*

Listing first 45 summaries
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Published Applications Nh:\*

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22: /cgn2\_6/ptodata/1/pubpna/USOP\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 6675, Ap	Sequence 2563, Ap	Sequence 7563, Ap	Sequence				-	Sequence 563, App	Sequence 5563, Ap	Sequence 10, Appl	
SUMMARIES	US-10-032-585-6675	US-10-128-714-2563	US-10-128-714-7563.	US-09-864-408A-2265	US-10-473-126-386	US-10-653-047-7103	US-10-128-714-1563	US-10-128-714-6563	US-10-128-714-563	US-10-128-714-5563	US-10-094-240-10	
	16	15	15	11	18	18	15	15	15	15	14	
* Query Match Length DB	2769	1992	1992	462	8056	. 688	2048	2048	4048	4048	4985	
& Query Match	78.6	5.1	5.1	3.3	3.3	3.3	3.5	3.5	3.5	3.5	3.0	
Score	2769	179.6	179.6	118	117.6	116.4	113.6	113.6	113.6	113.6	106.8	
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C 12 106.8 3.0 4985 16 US-10-056-405-10 106.2 3.0 575 18 US-10-653-047-447 27.4 2.7 969 18 US-10-653-047-447 94.4 2.7 969 18 US-10-363-345A-26081 94.4 2.7 969 18 US-10-363-345A-26081 95.6 2.6 90.4 2.7 969 18 US-10-363-345A-26081 95.6 2.6 90.6 2.6 90.6 19 US-10-363-345A-26081 95.6 2.6 90.6 19 US-10-363-345A-26081 95.6 2.6 90.6 19 US-10-363-345A-26081 95.6 2.6 90.6 18 US-10-973-126-240 95.6 2.5 80.6 18 US-10-073-126-240 95.6 2.5 80.6 18 US-10-9473-126-240 95.6 2.5 80.6 18 US-10-9473-126-240 95.6 18 US-10-9473-126-240 95.6 95.6 18 US-10-0473-126-240 95.6 95.6 18 US-10-0473-126-240 95.6 95.6 95.6 95.6 95.6 95.6 95.6 95.6	Sequence 10, Appl Sequence 447, App Sequence 137269				240	Sequence 240, App Sequence 151, App	10, 7	ñ,	Sequence 104. App	23	25	378,	2888		Sequence 28883, A		122		460, A	2130,	389, 7	142	46,	23,	Sequence 123, App	6714	89,
12 106.8 3.0 4985 14 94.4 2.8 575 16 94.4 2.7 969 17 94.4 2.7 969 18 92.6 2.7 969 19 92.6 2.6 8056 20 90. 2.6 8996 21 84.8 2.4 7676 22 84.8 2.4 7676 24 81.2 2.3 4985 25 79.6 2.3 3931 26 79.6 2.3 8759 27 78.2 2.2 8759 28 78.2 2.2 8759 29 78.2 2.2 8759 31 77.4 2.2 8759 32 77.4 2.2 535 34 77.4 2.2 535 35 77.4 2.2 535 36 74.6 2.1 15766 37 75.4 2.1 16766 39 74.6 2.1 16766 41 74.4 2.1 50000 42 73.4 2.1 83391 44 73.4 2.1 83391	10-056-405-10 10-653-047-447 10-425-115-13726	10-363-345A-2608 10-363-345A-2608	99	0-0	10-473-126-	10-473-126- 10-240-485-	2	22	10-473-126-	10-473-	10-473-	-	흐	9	-10-	-01	9	10-437-963-7	10-311-455-4	10-3	10-221-613-38	10-257-166-1	10-240-454-4	-10-706-635-	10-433-793-1	-10-032-585-6	-10-433-793-8
112 115 4 30 116 6 8 116 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	18 18 18	18 18	5 £	18	18	12 1	14	16	18	18	18	18	18	18	19	13	12	18	12	12	17	17	11	19	18	16	18
112 106.8 115 94.4.4.2 116 94.4.4.4.2 117 94.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	4985 575 286	696	696	3996	8056	7676	4985	3931	8759	8759	8759	8759	532	535	535	23	9	564	17183	16766	19380	7025	7025	50000	m	642	₹"
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	106.8 106.2 97.4	94.4	94.4 94.4		96.6	84.8 84.8	81.2		78.2	78.2	78.2	78.2	77.4	77.4	77.4	•		76.2	•			•	•	٠	Ė	73.4	73.4
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### ALIGNMENTS

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Discovery	Gaps .	GATCT	GATCT	ATAGT	ATAGT	AACAA
arget	2769;	TCCTA	rrccra	TAGTG	TAGTG	CGAAA
T guz		ACCTA:	ACCIA	rgcca,	rgcca1	AAAAA
for D		AATCA	AATCA	GATTG	GATTG	GTTGT
ogies	.DB 16;	CTACT	CTACT	CTAAT	CTAAT	CAGAA
hodold 85	0 0	TATTATCAAATTCAACTACTAATCAACCTATTCCTAGATCT	ATTCA	AAATC	AAATC	TAGAAT
2585 on Met	Score 2769; Pred. No. 0; ; Mismatches	VTCAAA	TCAAA	PAAATC	AAATC	AGAAT
//1003: A1 ruptic 9 US/10, 2-20	0	TTATT	TTATI	TCATAC	TCATAC	AAAATC
ULT 1  10-032-585-6675  equence 6675, Application US/10032585  ublication No. US20030180953A1  ENERAL INFORMATION:  ENERAL INFORMATION:  APPLICANT: Bo, Jang  APPLICANT: Bo, Jang  APPLICANT: Howard, Bussey  APPLICANT: HOWARD, Gene Disruption Methodologies for Drug Target  APPLICANT: HOWARD, Boone  APPLICANT: NUMERR: US/10/032,585  CURRENT APPLICATION NUMBER: US/10/032,585  CURRENT APPLICATION NUMBER: US/10/032,585  CURRENT APPLICATION NUMBER: US/10/032,585  CURRENT APPLICATION VERSION 3.1  ELENGTH: 2769  TYPE: DNA  ORGANISM: Candida albicans  10-032-585-6675	78.6%; 100.0%; tive	ATGTCCGATAGTGAAAGT	atgtccgatagtgaaagttattatcaaaattcaactactaaccaacc	GATGAAGTATTGGATGATCATAGAAATCAAATCACTAATGATTGTGCCATTAGTGATAGT	GATGAAGTATTGGATGATCATAGAAATCAAATCACTAATGATTGTGCCATTAGTGATAGT	Gaagatgagttggaattaaaatcagaattagaatcagaagttgtaaaaagcgaaaaacaa s17
Modern Street St	78. larity 100 Conservative	GATAG	GATAG	GTATT	GTATT	GAGTT
75. Application UNO. US2003018095 NNO. US2003018095 NNATION: Terry, Roemer D. Bo, Jang Charles, Boone Howard, Bussey VERTION: Gene Di NUCE: 1018-2005-9 LICATION NUMBER: LING DATE: 2001- SEQ ID NOS: 8000 SALENTIN VERSION 75 Candida albicans 6675	imilar ; Con	ATGTCC	ATGTCC	SATGAA	SATGAA	BAAGAT
0-022-585-66 0-032-585-66 Dilcation No NERAL INFORM PPLICANT: TE PPLICANT: B PPLICANT: H ITLE OF INVE URENT FILIN UMERY PILIN	latch cal S: 2769	338	7	398 (	61 (	458 (
RESULT 1 US-10-032-585-6675 Sequence 6675, Application US/10032585; Publication No. US20030180953A1 GENERAL INFORMATION: APPLICANT: Bob, Jiang APPLICANT: Charles, Boone APPLICANT: Howard, Bussey, TITLE REFERENCE: 10182-005-999 CURRENT APPLICATION NUMBER: US/10/032 CURRENT PILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 8000 SOFTWARE: PatentIn version 3.1 SEQ ID NO 6675 ILENGTH: 2769 TYPE: DNA CRANISM: Candida albicans US-10-032-585-6675	Query Match Best Local Similarity Matches 2769; Conser					
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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 1018-018-999
CURRENT PILING DATE: 2002-04-23
FRIOR PILING DATE: 2001-04-27
FRIOR PLICATION NUMBER: US 60/295,890
FRIOR FILING DATE: 2001-06-05
FRIOR PLICATION NUMBER: US 60/303,899
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 2563
LENGTH: 1992
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                                                                                                                                                                                                                                                                           GTCCCTGGTGAAGGTGCTACCAATTTAGGTTGGTTTTTTCGGAATTGTTGGAGTATTAATA 2580
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                                                         2341 AATTTATTAGCCTATGAAAAATTTTCAGTCGTTCATTTCAAATTATTAGCTCAATTA 2400
                                                                                                                                                                         ATTGGGACAATGTTAGTTCCATTAAATTTAGTCACGGGACTTTTTGGTATGAATGTAAGA 2857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-10-128-714-2563
Sequence 2563, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Aspergillus fumigatus
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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
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PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR PLICATION NUMBER: US 60/315,362
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Publication No. US20030119013A1
GENERAL INFORMATION:
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